

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: ANDERSON, Darrell R.  
HANNA, Nabil  
BRAMS, Peter
- (ii) TITLE OF INVENTION: IDENTIFICATION OF UNIQUE BINDING  
INTERACTIONS BETWEEN CERTAIN ANTIBODIES AND THE HUMAN B7.1  
AND B7.2 CO-STIMULATORY ANTIGENS
- (iii) NUMBER OF SEQUENCES: 6
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
  - (B) STREET: P.O. Box 1404
  - (C) CITY: Alexandria
  - (D) STATE: Virginia
  - (E) COUNTRY: United States
  - (F) ZIP: 22313-1404
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/746,361
  - (B) FILING DATE: 08-NOV-1996
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/487,550
  - (B) FILING DATE: 07-JUN-1995
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Teskin, Robin L.
  - (B) REGISTRATION NUMBER: 35,030
  - (C) REFERENCE/DOCKET NUMBER: 012712-256
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (703) 836-6620
  - (B) TELEFAX: (703) 836-2021

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 705 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..705
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG AGG GTC CCC GCT CAG CTC CTG GGG CTC CTG CTG CTC TGG CTC CCA  
Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Pro  
1 5 10 15

GGT	GCA	CGA	TGT	GCC	TAT	GAA	CTG	ACT	CAG	CCA	CCC	TCG	GTG	TCA	GTG	96
Gly	Ala	Arg	Cys	Ala	Tyr	Glu	Leu	Thr	Gln	Pro	Pro	Ser	Val	Ser	Val	
		20						25					30			
TCC	CCA	GGA	CAG	ACG	GCC	AGG	ATC	ACC	TGT	GGG	GGA	GAC	AAC	AGT	AGA	144
Ser	Pro	Gly	Gln	Thr	Ala	Arg	Ile	Thr	Cys	Gly	Gly	Asp	Asn	Ser	Arg	
		35					40					45				
AAT	GAA	TAT	GTC	CAC	TGG	TAC	CAG	CAG	AAG	CCA	GCG	CGG	GCC	CCT	ATA	192
Asn	Glu	Tyr	Val	His	Trp	Tyr	Gln	Gln	Lys	Pro	Ala	Arg	Ala	Pro	Ile	
	50					55					60					
CTG	GTC	ATC	TAT	GAT	GAT	AGT	GAC	CGG	CCC	TCA	GGG	ATC	CCT	GAG	CGA	240
Leu	Val	Ile	Tyr	Asp	Asp	Ser	Asp	Arg	Pro	Ser	Gly	Ile	Pro	Glu	Arg	
	65				70					75					80	
TTC	TCT	GGC	TCC	AAA	TCA	GGG	AAC	ACC	GCC	ACC	CTG	ACC	ATC	AAC	GGG	288
Phe	Ser	Gly	Ser	Lys	Ser	Gly	Asn	Thr	Ala	Thr	Leu	Thr	Ile	Asn	Gly	
				85					90					95		
GTC	GAG	GCC	GGG	GAT	GAG	GCT	GAC	TAT	TAC	TGT	CAG	GTG	TGG	GAC	AGG	336
Val	Glu	Ala	Gly	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Val	Trp	Asp	Arg	
			100					105					110			
GCT	AGT	GAT	CAT	CCG	GTC	TTC	GGA	GGA	GGG	ACC	CGG	GTG	ACC	GTC	CTA	384
Ala	Ser	Asp	His	Pro	Val	Phe	Gly	Gly	Gly	Thr	Arg	Val	Thr	Val	Leu	
		115					120					125				
GGT	CAG	CCC	AAG	GCT	GCC	CCC	TCG	GTC	ACT	CTG	TTC	CCG	CCC	TCC	TCT	432
Gly	Gln	Pro	Lys	Ala	Ala	Pro	Ser	Val	Thr	Leu	Phe	Pro	Pro	Ser	Ser	
	130					135					140					
GAG	GAG	CTT	CAA	GCC	AAC	AAG	GCC	ACA	CTG	GTG	TGT	CTC	ATA	AGT	GAC	480
Glu	Glu	Leu	Gln	Ala	Asn	Lys	Ala	Thr	Leu	Val	Cys	Leu	Ile	Ser	Asp	
	145				150					155					160	
TTC	TAC	CCG	GGA	GCC	GTG	ACA	GTG	GCC	TGG	AAG	GCA	GAT	AGC	AGC	CCC	528
Phe	Tyr	Pro	Gly	Ala	Val	Thr	Val	Ala	Trp	Lys	Ala	Asp	Ser	Ser	Pro	
				165					170					175		
GTC	AAG	GCG	GGA	GTG	GAG	ACC	ACC	ACA	CCC	TCC	AAA	CAA	AGC	AAC	AAC	576
Val	Lys	Ala	Gly	Val	Glu	Thr	Thr	Thr	Pro	Ser	Lys	Gln	Ser	Asn	Asn	
			180					185					190			
AAG	TAC	GCG	GCC	AGC	AGC	TAC	CTG	AGC	CTG	ACG	CCT	GAG	CAG	TGG	AAG	624
Lys	Tyr	Ala	Ala	Ser	Ser	Tyr	Leu	Ser	Leu	Thr	Pro	Glu	Gln	Trp	Lys	
		195					200					205				
TCC	CAC	AGA	AGC	TAC	AGC	TGC	CAG	GTC	ACG	CAT	GAA	GGG	AGC	ACC	GTG	672
Ser	His	Arg	Ser	Tyr	Ser	Cys	Gln	Val	Thr	His	Glu	Gly	Ser	Thr	Val	
		210				215					220					
GAG	AAG	ACA	GTG	GCC	CCT	ACA	GAA	TGT	TCA	TGA						705
Glu	Lys	Thr	Val	Ala	Pro	Thr	Glu	Cys	Ser	*						
	225				230					235						

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATG AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA GCT CCC AGA TGG	48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp	
240 245 250	
GTC CTG TCC GAG GTG AAG CTG CAG CAG TGG GGC GAA GGA CTT CTG CAG	96
Val Leu Ser Glu Val Lys Leu Gln Gln Trp Gly Glu Gly Leu Leu Gln	
255 260 265	
CCT TCG GAG ACC CTG TCC CGC ACC TGC GTT GTG TCT GGT GGC TCC ATC	144
Pro Ser Glu Thr Leu Ser Arg Thr Cys Val Val Ser Gly Gly Ser Ile	
270 275 280	
AGC GGT TAC TAC TAC TGG ACC TGG ATC CGC CAG ACC CCA GGG AGG GGA	192
Ser Gly Tyr Tyr Tyr Trp Thr Trp Ile Arg Gln Thr Pro Gly Arg Gly	
285 290 295	
CTG GAG TGG ATT GGC CAT ATT TAT GGT AAT GGT GCG ACC ACC AAC TAC	240
Leu Glu Trp Ile Gly His Ile Tyr Gly Asn Gly Ala Thr Thr Asn Tyr	
300 305 310 315	
AAT CCC TCC CTC AAG AGT CGA GTC ACC ATT TCA AAA GAC ACG TCC AAG	288
Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Thr Ser Lys	
320 325 330	
AAC CAG TTC TTC CTG AAC TTG AAT TCT GTG ACC GAC GCG GAC ACG GCC	336
Asn Gln Phe Phe Leu Asn Leu Asn Ser Val Thr Asp Ala Asp Thr Ala	
335 340 345	
GTC TAT TAC TGT GCG AGA GGC CCT CGC CCT GAT TGC ACA ACC ATT TGT	384
Val Tyr Tyr Cys Ala Arg Gly Pro Arg Pro Asp Cys Thr Thr Ile Cys	
350 355 360	
TAT GGC GGC TGG GTC GAT GTC TGG GGC CCG GGA GAC CTG GTC ACC GTC	432
Tyr Gly Gly Trp Val Asp Val Trp Gly Pro Gly Asp Leu Val Thr Val	
365 370 375	
TCC TCA GCT AGC ACC AAG GGC CCA TCG GTC TTC CCC CTG GCA CCC TCC	480
Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser	
380 385 390 395	
TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG GGC TGC CTG GTC AAG	528
Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys	
400 405 410	
GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA GGC GCC CTG	576
Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu	
415 420 425	
ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC	624
Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu	
430 435 440	
TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC	672
Tyr Ser Leu Ser Ser Val Thr Val Pro Ser Ser Ser Leu Gly Thr	
445 450 455	
CAG ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG	720
Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val	
460 465 470 475	

GAC Asp	AAG Lys	AAA Lys	GCA Ala	GAG Glu 480	CCC Pro	AAA Lys	TCT Ser	TGT Cys	GAC Asp 485	AAA Lys	ACT Thr	CAC His	ACA Thr	TGC Cys 490	CCA Pro	768
CCG Pro	TGC Cys	CCA Pro	GCA Ala 495	CCT Pro	GAA Glu	CTC Leu	CTG Leu	GGG Gly 500	GGA Gly	CCG Pro	TCA Ser	GTC Val	TTC Phe 505	CTC Leu	TTC Phe	816
CCC Pro	CCA Pro	AAA Lys 510	CCC Pro	AAG Lys	GAC Asp	ACC Thr	CTC Leu 515	ATG Met	ATC Ile	TCC Ser	CGG Arg	ACC Thr 520	CCT Pro	GAG Glu	GTC Val	864
ACA Thr	TGC Cys 525	GTG Val	GTG Val	GTG Val	GAC Asp	GTG Val 530	AGC Ser	CAC His	GAA Glu	GAC Asp	CCT Pro 535	GAG Glu	GTC Val	AAG Lys	TTC Phe	912
AAC Asn 540	TGG Trp	TAC Tyr	GTG Val	GAC Asp	GGC Gly 545	GTG Val	GAG Glu	GTG Val	CAT His	AAT Asn 550	GCC Ala	AAG Lys	ACA Thr	AAG Lys	CCG Pro 555	960
CGG Arg	GAG Glu	GAG Glu	CAG Gln 560	TAC Tyr	AAC Asn	AGC Ser	ACG Thr	TAC Tyr 565	CGT Arg	GTG Val	GTC Val	AGC Ser	GTC Val	CTC Leu 570	ACC Thr	1008
GTC Val	CTG Leu	CAC His	CAG Gln 575	GAC Asp	TGG Trp	CTG Leu	AAT Asn	GGC Gly 580	AAG Lys	GAG Glu	TAC Tyr	AAG Lys	TGC Cys 585	AAG Lys	GTC Val	1056
TCC Ser	AAC Asn	AAA Lys 590	GCC Ala	CTC Leu	CCA Pro	GCC Ala	CCC Pro 595	ATC Ile	GAG Glu	AAA Lys	ACC Thr	ATC Ile 600	TCC Ser	AAA Lys	GCC Ala	1104
AAA Lys 605	GGG Gly	CAG Gln	CCC Pro	CGA Arg	GAA Glu 610	CCA Pro	CAG Gln	GTG Val	TAC Tyr	ACC Thr	CTG Leu 615	CCC Pro	CCA Pro	TCC Ser	CGG Arg	1152
GAT Asp 620	GAG Glu	CTG Leu	ACC Thr	AAG Lys	AAC Asn 625	CAG Gln	GTC Val	AGC Ser	CTG Leu	ACC Thr 630	TGC Cys	CTG Leu	GTC Val	AAA Lys	GGC Gly 635	1200
TTC Phe	TAT Tyr	CCC Pro	AGC Ser	GAC Asp 640	ATC Ile	GCC Ala	GTG Val	GAG Glu	TGG Trp 645	GAG Glu	AGC Ser	AAT Asn	GGG Gly	CAG Gln 650	CCG Pro	1248
GAG Glu	AAC Asn	AAC Asn	TAC Tyr 655	AAG Lys	ACC Thr	ACG Thr	CCT Pro	CCC Pro 660	GTG Val	CTG Leu	GAC Asp	TCC Ser	GAC Asp 665	GGC Gly	TCC Ser	1296
TTC Phe	TTC Phe	CTC Leu 670	TAC Tyr	AGC Ser	AAG Lys	CTC Leu	ACC Thr 675	GTG Val	GAC Asp	AAG Lys	AGC Ser	AGG Arg 680	TGG Trp	CAG Gln	CAG Gln	1344
GGG Gly 685	AAC Asn	GTC Val	TTC Phe	TCA Ser	TGC Cys	TCC Ser 690	GTG Val	ATG Met	CAT His	GAG Glu	GCT Ala 695	CTG Leu	CAC His	AAC Asn	CAC His	1392
TAC Tyr 700	ACG Thr	CAG Gln	AAG Lys	AGC Ser	CTC Leu 705	TCC Ser	CTG Leu	TCT Ser	CCG Pro	GGT Gly 710	AAA Lys	TGA *				1431

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 720 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG AGC CTC CCT GCT CAG CTC CTC GGG CTG CTA TTG CTC TGC GTC CCC	48
Met Ser Leu Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Cys Val Pro	
480 485 490	
GGG TCC AGT GGG GAA GTT GTG ATG ACT CAG TCT CCA CTG TCC CTT CCC	96
Gly Ser Ser Gly Glu Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro	
495 500 505	
ATC ACA CCT GGA GAG CCG GCC TCC ATC TCC TGT AGG TCT AGT CAA AGC	144
Ile Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser	
510 515 520 525	
CTT AAA CAC AGT AAT GGA GAC ACC TTC CTG AGT TGG TAT CAG CAG AAG	192
Leu Lys His Ser Asn Gly Asp Thr Phe Leu Ser Trp Tyr Gln Gln Lys	
530 535 540	
CCA GGC CAA CCT CCA AGG CTC CTG ATT TAT AAG GTT TCT AAC CGG GAC	240
Pro Gly Gln Pro Pro Arg Leu Leu Ile Tyr Lys Val Ser Asn Arg Asp	
545 550 555	
TCT GGG GTC CCA GAC AGA TTC AGC GGC AGT GGG GCA GGG ACA GAT TTC	288
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe	
560 565 570	
ACA CTG AAA ATC AGC GCA GTG GAG GCT GAA GAT GTT GGG GTT TAT TTC	336
Thr Leu Lys Ile Ser Ala Glu Ala Glu Asp Val Gly Val Tyr Phe	
575 580 585	
TGC GGG CAA GGT ACA AGG ACT CCT CCC ACT TTC GGC GGA GGG ACC AAG	384
Cys Gly Gln Gly Thr Arg Thr Pro Pro Thr Phe Gly Gly Gly Thr Lys	
590 595 600 605	
GTG GAA ATC AAA CGT ACG GTG GCT GCA CCA TCT GTC TTC ATC TTC CCG	432
Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro	
610 615 620	
CCA TCT GAT GAG CAG TTG AAA TCT GGA ACT GCC TCT GTT GTG TGC CTG	480
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu	
625 630 635	
CTG AAT AAC TTC TAT CCC AGA GAG GCC AAA GTA CAG TGG AAG GTG GAT	528
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp	
640 645 650	
AAC GCC CTC CAA TCG GGT AAC TCC CAG GAG AGT GTC ACA GAG CAG GAC	576
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp	
655 660 665	
AGC AAG GAC AGC ACC TAC AGC CTC AGC AGC ACC CTG ACG CTG AGC AAA	624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys	
670 675 680 685	
GCA GAC TAC GAG AAA CAC AAA GTC TAC GCC TGC GAA GTC ACC CAT CAG	672
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln	
690 695 700	

GGC	CTG	AGC	TCG	CCC	GTC	ACA	AAG	AGC	TTC	AAC	AGG	GGA	GAG	TGT	TGA	720
Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys	*	
			705					710					715			

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATG	GGT	TGG	AGC	CTC	ATC	TTG	CTC	TTC	CTT	GTC	GCT	GTT	GCT	ACG	CGT	48
Met	Gly	Trp	Ser	Leu	Ile	Leu	Leu	Phe	Leu	Val	Ala	Val	Ala	Thr	Arg	
			245					250						255		
GTC	CAG	TGT	GAG	GTG	CAA	CTG	GTG	GAG	TCT	GGG	GGA	GGC	TTG	GTC	CAG	96
Val	Gln	Cys	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	
			260					265					270			
CCT	GGC	GGG	TCC	CTG	AGA	GTC	TCC	TGT	GCA	GTC	TCT	GGA	TTC	ACC	TTC	144
Pro	Gly	Gly	Ser	Leu	Arg	Val	Ser	Cys	Ala	Val	Ser	Gly	Phe	Thr	Phe	
			275				280					285				
AGT	GAC	CAC	TAC	ATG	TAT	TGG	TTC	CGC	CAG	GCT	CCA	GGG	AAG	GGG	CCG	192
Ser	Asp	His	Tyr	Met	Tyr	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Pro	
	290					295					300					
GAA	TGG	GTA	GGT	TTC	ATT	AGA	AAC	AAA	CCG	AAC	GGT	GGG	ACA	ACA	GAA	240
Glu	Trp	Val	Gly	Phe	Ile	Arg	Asn	Lys	Pro	Asn	Gly	Gly	Thr	Thr	Glu	
	305				310				315						320	
TAC	GCC	GCG	TCT	GTG	AAA	GAC	AGA	TTC	ACC	ATC	TCC	AGA	GAT	GAT	TCC	288
Tyr	Ala	Ala	Ser	Val	Lys	Asp	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	
				325					330					335		
AAA	AGC	ATC	GCC	TAT	CTG	CAA	ATG	AGC	AGC	CTG	AAA	ATC	GAG	GAC	ACG	336
Lys	Ser	Ile	Ala	Tyr	Leu	Gln	Met	Ser	Ser	Leu	Lys	Ile	Glu	Asp	Thr	
			340					345					350			
GCC	GTC	TAT	TAC	TGT	ACT	ACA	TCC	TAC	ATT	TCA	CAT	TGT	CGG	GGT	GGT	384
Ala	Val	Tyr	Tyr	Cys	Thr	Thr	Ser	Tyr	Ile	Ser	His	Cys	Arg	Gly	Gly	
			355				360					365				
GTC	TGC	TAT	GGA	GGT	TAC	TTC	GAA	TTC	TGG	GGC	CAG	GGC	GCC	CTG	GTC	432
Val	Cys	Tyr	Gly	Gly	Tyr	Phe	Glu	Phe	Trp	Gly	Gln	Gly	Ala	Leu	Val	
	370				375						380					
ACC	GTC	TCC	TCA	GCT	AGC	ACC	AAG	GGC	CCA	TCG	GTC	TTC	CCC	CTG	GCA	480
Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	
				385		390				395				400		
CCC	TCC	TCC	AAG	AGC	ACC	TCT	GGG	GGC	ACA	GCG	GCC	CTG	GGC	TGC	CTG	528
Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	
			405					410						415		

GTC	AAG	GAC	TAC	TTC	CCC	GAA	CCG	GTG	ACG	GTG	TCG	TGG	AAC	TCA	GGC	576
Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	
		420						425					430			
GCC	CTG	ACC	AGC	GGC	GTG	CAC	ACC	TTC	CCG	GCT	GTC	CTA	CAG	TCC	TCA	624
Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	
		435					440					445				
GGA	CTC	TAC	TCC	CTC	AGC	AGC	GTG	GTG	ACC	GTG	CCC	TCC	AGC	AGC	TTG	672
Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	
	450					455					460					
GGC	ACC	CAG	ACC	TAC	ATC	TGC	AAC	GTG	AAT	CAC	AAG	CCC	AGC	AAC	ACC	720
Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	
465					470					475					480	
AAG	GTG	GAC	AAG	AAA	GCA	GAG	CCC	AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	768
Lys	Val	Asp	Lys	Lys	Ala	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	
				485					490					495		
TGC	CCA	CCG	TGC	CCA	GCA	CCT	GAA	CTC	CTG	GGG	GGA	CCG	TCA	GTC	TTC	816
Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	
			500					505					510			
CTC	TTC	CCC	CCA	AAA	CCC	AAG	GAC	ACC	CTC	ATG	ATC	TCC	CGG	ACC	CCT	864
Leu	Phe		Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	
		515					520					525				
GAG	GTC	ACA	TGC	GTG	GTG	GTG	GAC	GTG	AGC	CAC	GAA	GAC	CCT	GAG	GTC	912
Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	
	530					535					540					
AAG	TTC	AAC	TGG	TAC	GTG	GAC	GGC	GTG	GAG	GTG	CAT	AAT	GCC	AAG	ACA	960
Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	
545					550					555					560	
AAG	CCG	CGG	GAG	GAG	CAG	TAC	AAC	AGC	ACG	TAC	CGT	GTG	GTC	AGC	GTC	1008
Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	
				565					570					575		
CTC	ACC	GTC	CTG	CAC	CAG	GAC	TGG	CTG	AAT	GGC	AAG	GAG	TAC	AAG	TGC	1056
Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	
			580					585					590			
AAG	GTC	TCC	AAC	AAA	GCC	CTC	CCA	GCC	CCC	ATC	GAG	AAA	ACC	ATC	TCC	1104
Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	
		595					600					605				
AAA	GCC	AAA	GGG	CAG	CCC	CGA	GAA	CCA	CAG	GTG	TAC	ACC	CTG	CCC	CCA	1152
Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	
	610					615					620					
TCC	CGG	GAT	GAG	CTG	ACC	AAG	AAC	CAG	GTC	AGC	CTG	ACC	TGC	CTG	GTC	1200
Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	
625					630					635					640	
AAA	GGC	TTC	TAT	CCC	AGC	GAC	ATC	GCC	GTG	GAG	TGG	GAG	AGC	AAT	GGG	1248
Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	
				645					650					655		
CAG	CCG	GAG	AAC	AAC	TAC	AAG	ACC	ACG	CCT	CCC	GTG	CTG	GAC	TCC	GAC	1296
Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	
			660					665					670			
GGC	TCC	TTC	TTC	CTC	TAC	AGC	AAG	CTC	ACC	GTG	GAC	AAG	AGC	AGG	TGG	1344
Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	
		675					680					685				

CAG	CAG	GGG	AAC	GTC	TTC	TCA	TGC	TCC	GTG	ATG	CAT	GAG	GCT	CTG	CAC	1392
Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	
690						695					700					

AAC	CAC	TAC	ACG	CAG	AAG	AGC	CTC	TCC	CTG	TCT	CCG	GGT	AAA	TGA		1437
Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys	*		
705					710					715						

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 711 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG	AGG	GTC	CCC	GCT	CAG	CTC	CTG	GGG	CTC	CTG	CTG	CTC	TGG	CTC	CCA	48
Met	Arg	Val	Pro	Ala	Gln	Leu	Leu	Gly	Leu	Leu	Leu	Leu	Trp	Leu	Pro	
480					485					490					495	
GGT	GCA	CGA	TGT	GAG	TCT	GTC	CTG	ACA	CAG	CCG	CCC	TCA	GTG	TCT	GGG	96
Gly	Ala	Arg	Cys	Glu	Ser	Val	Leu	Thr	Gln	Pro	Pro	Ser	Val	Ser	Gly	
				500					505					510		
GCC	CCA	GGG	CAG	AAG	GTC	ACC	ATC	TCG	TGC	ACT	GGG	AGC	ACC	TCC	AAC	144
Ala	Pro	Gly	Gln	Lys	Val	Thr	Ile	Ser	Cys	Thr	Gly	Ser	Thr	Ser	Asn	
			515					520					525			
ATT	GGA	GGT	TAT	GAT	CTA	CAT	TGG	TAC	CAG	CAG	CTC	CCA	GGA	ACG	GCC	192
Ile	Gly	Gly	Tyr	Asp	Leu	His	Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Thr	Ala	
		530					535					540				
CCC	AAA	CTC	CTC	ATC	TAT	GAC	ATT	AAC	AAG	CGA	CCC	TCA	GGA	ATT	TCT	240
Pro	Lys	Leu	Leu	Ile	Tyr	Asp	Ile	Asn	Lys	Arg	Pro	Ser	Gly	Ile	Ser	
	545					550					555					
GAC	CGA	TTC	TCT	GGC	TCC	AAG	TCT	GGT	ACC	GCG	GCC	TCC	CTG	GCC	ATC	288
Asp	Arg	Phe	Ser	Gly	Ser	Lys	Ser	Gly	Thr	Ala	Ala	Ser	Leu	Ala	Ile	
560				565						570					575	
ACT	GGG	CTC	CAG	ACT	GAG	GAT	GAG	GCT	GAT	TAT	TAC	TGC	CAG	TCC	TAT	336
Thr	Gly	Leu	Gln	Thr	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Ser	Tyr	
			580					585						590		
GAC	AGC	AGC	CTG	AAT	GCT	CAG	GTA	TTC	GGA	GGA	GGG	ACC	CGG	CTG	ACC	384
Asp	Ser	Ser	Leu	Asn	Ala	Gln	Val	Phe	Gly	Gly	Gly	Thr	Arg	Leu	Thr	
			595				600						605			
GTC	CTA	GGT	CAG	CCC	AAG	GCT	GCC	CCC	TCG	GTC	ACT	CTG	TTC	CCG	CCC	432
Val	Leu	Gly	Gln	Pro	Lys	Ala	Ala	Pro	Ser	Val	Thr	Leu	Phe	Pro	Pro	
		610					615					620				
TCC	TCT	GAG	GAG	CTT	CAA	GCC	AAC	AAG	GCC	ACA	CTG	GTG	TGT	CTC	ATA	480
Ser	Ser	Glu	Glu	Leu	Gln	Ala	Asn	Lys	Ala	Thr	Leu	Val	Cys	Leu	Ile	
		625				630					635					



AGT GAC TTC TAC CCG GGA GCC GTG ACA GTG GCC TGG AAG GCA GAT AGC	528
Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser	
640 645 650 655	
AGC CCC GTC AAG GCG GGA GTG GAG ACC ACC ACA CCC TCC AAA CAA AGC	576
Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser	
660 665 670	
AAC AAC AAG TAC GCG GCC AGC AGC TAC CTG AGC CTG ACG CCT GAG CAG	624
Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln	
675 680 685	
TGG AAG TCC CAC AGA AGC TAC AGC TGC CAG GTC ACG CAT GAA GGG AGC	672
Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser	
690 695 700	
ACC GTG GAG AAG ACA GTG GCC CCT ACA GAA TGT TCA TGA	711
Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser *	
705 710 715	

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATG AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA GCT CCC AGA TGG	48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp	
240 245 250	
GTC CTG TCC CAG GTG CAG CTG CAG GAG TCG GGC CCA GGA CTG GTG AAG	96
Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys	
255 260 265	
CCT TCG GAG ACC CTG TCC CTC ACC TGC GCT GTC TCT GGT GGC TCC ATC	144
Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile	
270 275 280 285	
AGC GGT GGT TAT GGC TGG GGC TGG ATC CGC CAG CCC CCA GGG AAG GGG	192
Ser Gly Gly Tyr Gly Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly	
290 295 300	
CTG GAG TGG ATT GGG AGT TTC TAT AGT AGT AGT GGG AAC ACC TAC TAC	240
Leu Glu Trp Ile Gly Ser Phe Tyr Ser Ser Ser Gly Asn Thr Tyr Tyr	
305 310 315	
AAC CCC TCC CTC AAG AGT CAA GTC ACC ATT TCA ACA GAC ACG TCC AAG	288
Asn Pro Ser Leu Lys Ser Gln Val Thr Ile Ser Thr Asp Thr Ser Lys	
320 325 330	
AAC CAG TTC TCC CTG AAG CTG AAC TCT ATG ACC GCC GCG GAC ACG GCC	336
Asn Gln Phe Ser Leu Lys Leu Asn Ser Met Thr Ala Ala Asp Thr Ala	
335 340 345	

GTG	TAT	TAC	TGT	GTG	AGA	GAT	CGT	CTT	TTT	TCA	GTT	GTT	GGA	ATG	GTT	384
Val	Tyr	Tyr	Cys	Val	Arg	Asp	Arg	Leu	Phe	Ser	Val	Val	Gly	Met	Val	
350					355					360					365	
TAC	AAC	AAC	TGG	TTC	GAT	GTC	TGG	GGC	CCG	GGA	GTC	CTG	GTC	ACC	GTC	432
Tyr	Asn	Asn	Trp	Phe	Asp	Val	Trp	Gly	Pro	Gly	Val	Leu	Val	Thr	Val	
				370					375					380		
TCC	TCA	GCT	AGC	ACC	AAG	GGC	CCA	TCG	GTC	TTC	CCC	CTG	GCA	CCC	TCC	480
Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	
			385					390					395			
TCC	AAG	AGC	ACC	TCT	GGG	GGC	ACA	GCG	GCC	CTG	GGC	TGC	CTG	CTC	AAG	528
Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Leu	Lys	
		400					405					410				
GAC	TAC	TTC	CCC	GAA	CCG	GTG	ACG	GTG	TCG	TGG	AAC	TCA	GGC	GCC	CTG	576
Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	
	415					420					425					
ACC	AGC	GGC	GTG	CAC	ACC	TTC	CCG	GCT	GTC	CTA	CAG	TCC	TCA	GGA	CTC	624
Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	
430					435					440					445	
TAC	TCC	CTC	AGC	AGC	GTG	GTG	ACC	GTG	CCC	TCC	AGC	AGC	TTG	GGC	ACC	672
Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	
				450					455					460		
CAG	ACC	TAC	ATC	TGC	AAC	GTG	AAT	CAC	AAG	CCC	AGC	AAC	ACC	AAG	GTG	720
Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	
			465					470					475			
GAC	AAG	AAA	GCA	GAG	CCC	AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	CCA	768
Asp	Lys	Lys	Ala	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	
		480					485					490				
CCG	TGC	CCA	GCA	CCT	GAA	CTC	CTG	GGG	GGA	CCG	TCA	GTC	TTC	CTC	TTC	816
Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	
	495					500					505					
CCC	CCA	AAA	CCC	AAG	GAC	ACC	CTC	ATG	ATC	TCC	CGG	ACC	CCT	GAG	GTC	864
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	
510				515						520					525	
ACA	TGC	GTG	GTG	GTG	GAC	GTG	AGC	CAC	GAA	GAC	CCT	GAG	GTC	AAG	TTC	912
Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	
				530					535					540		
AAC	TGG	TAC	GTG	GAC	GGC	GTG	GAG	GTG	CAT	AAT	GCC	AAG	ACA	AAG	CCG	960
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	
			545				550						555			
CGG	GAG	GAG	CAG	TAC	AAC	AGC	ACG	TAC	CGT	GTG	GTC	AGC	GTC	CTC	ACC	1008
Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	
		560					565					570				
GTC	CTG	CAC	CAG	GAC	TGG	CTG	AAT	GGC	AAG	GAG	TAC	AAG	TGC	AAG	GTC	1056
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	
	575					580					585					
TCC	AAC	AAA	GCC	CTC	CCA	GCC	CCC	ATC	GAG	AAA	ACC	ATC	TCC	AAA	GCC	1104
Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	
590					595					600					605	
AAA	GGG	CAG	CCC	CGA	GAA	CCA	CAG	GTG	TAC	ACC	CTG	CCC	CCA	TCC	CGG	1152
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	
				610					615					620		

GAT	GAG	CTG	ACC	AAG	AAC	CAG	GTC	AGC	CTG	ACC	TGC	CTG	GTC	AAA	GGC	1200
Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	
			625					630					635			
TTC	TAT	CCC	AGC	GAC	ATC	GCC	GTG	GAG	TGG	GAG	AGC	AAT	GGG	CAG	CCG	1248
Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	
		640					645					650				
GAG	AAC	AAC	TAC	AAG	ACC	ACG	CCT	CCC	GTG	CTG	GAC	TCC	GAC	GGC	TCC	1296
Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	
	655					660					665					
TTC	TTC	CTC	TAC	AGC	AAG	CTC	ACC	GTG	GAC	AAG	AGC	AGG	TGG	CAG	CAG	1344
Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	
670					675					680					685	
GGG	AAC	GTC	TTC	TCA	TGC	TCC	GTG	ATG	CAT	GAG	GCT	CTG	CAC	AAC	CAC	1392
Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	
				690					695					700		
TAC	ACG	CAG	AAG	AGC	CTC	TCC	CTG	TCT	CCG	GGT	AAA	TGA				1431
Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys	*				
			705					710								